

SEQUENCE LISTING

<110> Saha, K.

<120> Methods and Materials Relating to CD8-Tropic HIV-1

<130> 28335/37036 US

<150> US 60/258,472

<151> 2000-12-28

<160> 27

<170> PatentIn version 3.1

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Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Ser Thr Glu Val
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His Asn Ile Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Ser Pro
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Gln Glu Ile Val Met Glu Asn Val Thr Glu Glu Phe Asn Met Trp Lys
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Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
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Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
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Arg Leu Ile Ser Cys Asn Thr Ser Ile Ile Thr Gln Ala Cys Pro Lys
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Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe
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Gly Gly Asp Pro Glu Ile Thr Met His Thr Phe Asn Cys Gly Gly Glu
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Phe Phe Tyr Cys Asn Thr Thr Gln Leu Phe Asn Ser Thr Trp Ile Arg
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Asn Gly Thr Asp Trp Thr Gln Asn Asp Thr Glu Gly Ser Asp Ile Thr
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Asn Glu Asn Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met
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Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln
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Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
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Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
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Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
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Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Lys
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Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr Asn Val Ser Thr
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Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu
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Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Val Asn
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Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu Asn Thr Ser Val
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Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Arg Ile Arg
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Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala Met Tyr Ala
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Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu
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Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu Ser Glu Ile Phe
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Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr
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Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His
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Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln
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Glu Val Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn
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Ser Phe Asn Val Thr Thr Leu Ile Arg Asn Lys Arg Lys Thr Glu Tyr
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Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala
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Gly Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Asn Gly Lys Gly
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Pro Cys Lys Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro
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Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Asp
260 265 270

Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala Lys Asn Ile Ile
275 280 285

Val Gln Leu Asn Val Ser Leu Glu Ile Asn Cys Thr Arg Pro Asn Asn
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Glu Ile Lys Gln Phe Lys Asn Lys Thr Ile Val Phe Lys Gln Ser Ser
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Gly Gly Asp Phe Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu
370 375 380

Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp His Ala
385 390 395 400

Asn Gly Thr Trp Lys Asn Thr Glu Gly Ala Asp Asn Asn Ile Thr Leu
405 410 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Gln Glu Val Gly Lys
420 425 430

Ala Met Tyr Ala Pro Pro Ile Glu Gly Gln Ile Arg Cys Leu Ser Asn
 435 440 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Ser Ser Glu Glu Asn
 450 455 460

Gln Thr Glu
 465

<210> 9
 <211> 2553
 <212> DNA
 <213> HIV-1

<400> 9
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 gtcacagttt attatggggt acctgtgtgg aaagaagcaa ccactactct attttgtgca 180
 tcagatgcta aatcatatga accagaggca cataatatct gggctacaca tgctgtgtg 240
 ccaacagacc ccaaccacg agaaataaaa ctggaaaatg tcacagaaaa ctttaacatg 300
 tggaaaaatg acatggtgga gcagatgcat gaggatgtaa tcagtctatg ggatcaaagc 360
 ctgaaaccat gtgtaaaatt aacccactc tgtgtcactt tacattgcac tgaatataag 420
 gccctaatag ccactattaa tgccactgat agggacatag gaatgaaaaa ctgctcttcc 480
 aatgtaacca cagaagtaat aaataagaag aagcaagaac atgcactttt ttataaactt 540
 gatgtggtac aaatggatga taatagtact aataccaact atagattaat aaattgtaat 600
 acctcagtca ttacacaggc gtgtccaaag gtaacctttg agccaattcc catacattat 660
 tgtgctccag ctggatttgc gattctaaag tgtaatgata agaagttcaa tgggacgggt 720
 ccatgcaaaa acgtcagcac agtgcagtgt acacatggga ttaggccagt agtgtcaacc 780
 caactgttgt tgaatggcag tctagcagaa gaagagataa taattagatc tgaatatctc 840
 acaaataatg ctaaaaccat aatagtacag cttaatgagt ctgtaccaat taattgctca 900
 aggccctacg aaaataaaaag acgacgtaca cctataggac tagggcaagc gtactataca 960
 acaaaattaa aaggatatat aagaccagca cattgtaata ttagtgaggc agaatggaat 1020
 aaaactttac aacaggtagc taaaaaatta ggagacctt tcaaccagac aacaataatt 1080
 tttaaccac actcgggagg ggaccagaa attacaacac acagctttaa ttgtggaggg 1140
 gaatttttct actgcgatac atcaagactg tttaatagga cttataatac atcaggtagt 1200
 acaggggtaa ataacagtac aatcaaactc ccatgcagaa taaaacaaat tataaacatg 1260
 tggcaggagg taggaaaagc aatgtatgcc cctcccattg aaggactaat caaatgttca 1320
 tcaaacatta caggactatt gttgacaaga gatgggggaa ataatactag gcagaatgaa 1380

gccttcaggc ctggaggagg ggatatgaga gacaattgga gaagtgaatt atacaaatat 1440
aaagtagtaa gaattgaacc actaggtcta gcacccactg aggcaaagag aagagtggta 1500
gaaagagaaa aaagagcaat aggactagga gctatgttcc ttgggttctt gggagcagca 1560
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gctgtgccct ggaactctag ctggagtaat aaatctctaa acgagatttg gggtaacatg 1860
acctggatgg agtgggaaaa agaaattgac aattacacag aattaatata cagcttaatt 1920
gaagaatcgc aaaccagca agaaaagaat gaacaagaac tattgaaatt agaccaatgg 1980
gcaagtttgt ggaattgggt tagcataaca aaatggctgt ggtatataaa aatattcata 2040
atgatagtag gaggcttgat aggtttaaga atagtttttg ctgtgctttc tgtagtaaatt 2100
agagttaggc agggatattc acctctgtca tttcagaccc tcctcccagc cccgagggga 2160
cccagacaggc cagaaggaat agaagaagaa ggtggagagc agggcagagg cagatccatt 2220
cgattgggtga ccggttctc agcacttata tgggacgata taaggaacct gtgcctcttc 2280
agctaccgcc acttgagaga cttaattctta attgcagcga agattgtgga gtttctggga 2340
cgcaggggggt gagaagccat caagtacctg tggaacctcc tgcaatattg gattcaggaa 2400
ctaaagaata gtgctattag cttatttgat accacagcaa tagcagtagc tgaggggaca 2460
gatagggtca tagagatatt acaaagattt attagagcta ttcttcacat acccagacga 2520
ataagacagg gcttggaag ggctttacta taa 2553

<210> 10
<211> 781
<212> PRT
<213> HIV-1

<400> 10
Met Arg Val Lys Ile Glu Arg Asn Tyr Gln His Leu Trp Glu Arg Asn
1 5 10 15

Gln His Ser Leu Trp Arg Trp Gly Ile Met Leu Leu Gly Met Leu Met
20 25 30

Ile Cys Lys Gly Glu Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val
35 40 45

Trp Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ser
50 55 60

Tyr Glu Pro Glu Ala His Asn Ile Trp Ala Thr His Ala Cys Val Pro
65 70 75 80

Thr Asp Pro Asn Pro Arg Glu Ile Lys Leu Glu Asn Val Thr Glu Asn
85 90 95

Phe Asn Met Trp Lys Asn Asp Met Val Glu Gln Met His Glu Asp Val
100 105 110

Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
115 120 125

Leu Cys Val Thr Leu His Cys Thr Glu Tyr Lys Ala Pro Asn Ala Thr
130 135 140

Ile Asn Ala Thr Asp Arg Asp Ile Gly Met Lys Asn Cys Ser Phe Asn
145 150 155 160

Val Thr Thr Glu Val Ile Asn Lys Lys Lys Gln Glu His Ala Leu Phe
165 170 175

Tyr Lys Leu Asp Val Val Gln Met Asp Asp Asn Ser Thr Asn Thr Asn
180 185 190

Tyr Arg Leu Ile Asn Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro
195 200 205

Lys Val Thr Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly
210 215 220

Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Asn Gly Thr Gly Pro
225 230 235 240

Cys Lys Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val
245 250 255

Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Ile
260 265 270

Ile Ile Arg Ser Glu Asn Leu Thr Asn Asn Ala Lys Thr Ile Ile Val
275 280 285

Gln Leu Asn Glu Ser Val Pro Ile Asn Cys Ser Arg Pro Tyr Glu Asn
290 295 300

Lys Arg Arg Arg Thr Pro Ile Gly Leu Gly Gln Tyr Tyr Thr Thr Lys
305 310 315 320

Leu Lys Gly Tyr Ile Arg Pro Ala His Cys Asn Ile Ser Gly Ala Glu
325 330 335

Trp Asn Lys Thr Leu Gln Gln Val Ala Lys Lys Leu Gly Asp Leu Phe
340 345 350

Asn Gln Thr Thr Ile Ile Phe Gln Pro His Ser Gly Gly Asp Pro Glu
355 360 365

Ile Thr Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp
370 375 380

Thr Ser Arg Leu Phe Asn Arg Thr Tyr Ser Thr Ser Gly Ser Thr Gly
385 390 395 400

Val Asn Asn Ser Thr Ile Lys Leu Pro Cys Arg Ile Lys Gln Ile Ile
405 410 415

Asn Met Trp Gln Gly Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Glu
420 425 430

Gly Leu Ile Lys Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg
435 440 445

Asp Gly Gly Asn Asn Thr Arg Gln Asn Glu Ala Phe Arg Pro Gly Gly
450 455 460

Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val
465 470 475 480

Val Arg Ile Glu Pro Leu Gly Leu Ala Pro Thr Glu Ala Lys Arg Arg
485 490 495

Val Val Glu Arg Glu Lys Arg Ala Ile Gly Leu Gly Ala Met Phe Leu
500 505 510

Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr
515 520 525

Leu Thr Val Gln Ala Arg Gln Leu Met Ser Gly Ile Val Gln Gln Gln
530 535 540

Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Thr
545 550 555 560

Leu Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu
565 570 575

Ser Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly
580 585 590

Arg His Ile Cys Thr Thr Ala Val Pro Trp Asn Ser Ser Trp Ser Asn
595 600 605

Lys Ser Leu Asn Glu Ile Trp Gly Asn Met Thr Trp Met Glu Trp Glu
610 615 620

Lys Glu Ile Asp Asn Tyr Thr Glu Leu Ile Tyr Ser Leu Ile Glu Glu
625 630 635 640

Ser Gln Thr Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Lys Leu Asp
645 650 655

Gln Trp Ala Ser Leu Trp Asn Trp Phe Ser Ile Thr Lys Trp Leu Trp
660 665 670

Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg
675 680 685

Ile Val Phe Ala Val Leu Ser Val Val Asn Arg Val Arg Gln Gly Tyr
690 695 700

Ser Pro Leu Ser Phe Gln Thr Leu Leu Pro Ala Pro Arg Gly Pro Asp
705 710 715 720

Arg Pro Glu Gly Ile Glu Glu Glu Gly Gly Glu Gln Gly Arg Gly Arg
725 730 735

Ser Ile Arg Leu Val Thr Gly Phe Ser Ala Leu Ile Trp Asp Asp Leu
740 745 750

Arg Asn Leu Cys Leu Phe Ser Tyr Arg His Leu Arg Asp Leu Ile Leu
755 760 765

Ile Ala Ala Lys Ile Val Glu Phe Leu Gly Arg Arg Gly
770 775 780

<210> 11
<211> 2586
<212> DNA
<213> HIV-1

<400> 11
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ttgggtatga tgataatttg tagtgctgca gaaaaattgt gggttactgt ttactatggg 120
gtacctgtgt ggaaagatgc agaaaccacc ttattttgtg catcagatgc gaaagcatat 180

gatacagaag	tgcataatgt	ctgggccaca	catgcctgtg	tacctacaga	ccccaaccca	240
caagaaataa	atttggaata	tgtgacagaa	aattttaaca	tgtggaaaaa	taacatggta	300
gagcagatgc	atacagatat	aatcagtcta	tgggaccaa	gcctaaagcc	atgtgtacag	360
ttaacccctc	tctgtgttac	tttagattgt	actgatgcca	caaatgccac	taataccact	420
atcatttagt	acatgaaagg	agaaataaaa	aactgctctt	tcaatatgac	cacagaatta	480
aaggataaga	cacagaaagt	acgttcattt	ttctataaga	tggatatagt	acaaattaac	540
aacaacaaca	gcaacagcaa	cagtagtcag	tatagattaa	taagttgtaa	tacctcaacc	600
attacacaag	cttgtccaaa	ggatctcttt	gagccaattc	ccatacatta	ttgtgctcca	660
gctgggtttg	cgattctaaa	atgcaaggat	aaggagttca	atggaacagg	gccatgcagg	720
aatgtcagca	cagtacaatg	cacacatgga	atcaagccag	tagtatcaac	tcaactactg	780
ttaaattggc	gtctagcaga	agaaaaggta	atgattagat	ctgaaaatat	cacagacaat	840
actaaaaaca	taatagtgc	acttactgag	cctgtaaaaa	ttaattgtac	cagacctaac	900
aacaatacaa	gaagaggtat	aagtataggg	ccaggacgag	cattcattgc	aagagataga	960
ataatagggg	atataagaca	agcacattgt	aacatcagta	gagcagcatg	gaataacact	1020
ttgcagaagg	tagcccaaca	attaagaaca	cactttgaga	acagaacaat	aatctttaat	1080
cactccgcag	gaggggaccc	agaaataact	acacatagtt	ttaattgtgg	aggagaattt	1140
ttctattgta	gcacaacagg	cctgtttaat	agtacttgga	atagcaatgc	cagcacgcag	1200
gggtcaaata	gcacgggttc	aaacgacact	ataactctcc	aatgcagaat	aaggcagatt	1260
ataaggatgt	ggcagagagt	aggacaagca	atgtatgccc	ctcccatccc	aggggtaata	1320
agatgtgact	caaacattac	aggactaata	ttaacaagag	atggggggga	taataacagc	1380
acaaatgaga	ccttcagacc	tggaggagga	gatatgaggg	acaattggag	aagtgaatta	1440
tataagtata	aagtagtaaa	gattgaacca	ctaggagtag	caccaccag	ggcaaagaga	1500
agagtgggtg	aaagagaaaa	aagagcaata	gcaggaatag	gagctgtgtt	ccttgggttc	1560
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cagctattgt	ctggcatagt	gcaacagcaa	agcaatttgc	tgagggttat	agaggctcaa	1680
cagcatctgt	tgaaactcac	ggtctggggc	attaacagc	tccaggcacg	agtccctggc	1740
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atgtgcacca	ctactgtgcc	ctggaactct	agttggagta	ataaatccta	tagtgagata	1860
tgggacaaca	tgacctggct	gcaatgggat	aaagaaatta	gcaattatac	acaaataata	1920
tatgatctaa	ttgaagaatc	acagaaccag	caggaaaaga	atgaacaaga	cctattggca	1980
ttggacaagt	gggcaaactc	atggaattgg	tttgacatat	caaaatggct	gtggtatata	2040
agaatattta	taatgatagt	aggaggctta	ataggattaa	gaatagtttt	tgctgtaatt	2100

tcagtaataa atagagttag gcagggatac tcacctttgt cgttccagac ccttgccccg 2160
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gataccatag caatagtaat agctggctgg acagataggg tcatagaaat aggacaaaga 2520
attggtagag ctattctcaa catacctaga agaatcaggc agggcgccga aagggtttta 2580
caataa 2586

<210> 12
<211> 861
<212> PRT
<213> HIV-1

<400> 12

Met Arg Val Lys Ile Gln Arg Asn Cys Gln Asn Leu Trp Arg Trp Gly
1 5 10 15

Thr Ile Ile Leu Gly Met Met Ile Ile Cys Ser Ala Ala Glu Lys Leu
20 25 30

Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Asp Ala Glu Thr
35 40 45

Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His
50 55 60

Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln
65 70 75 80

Glu Ile Asn Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn
85 90 95

Asn Met Val Glu Gln Met His Thr Asp Ile Ile Ser Leu Trp Asp Gln
100 105 110

Ser Leu Lys Pro Cys Val Gln Leu Thr Pro Leu Cys Val Thr Leu Asp
115 120 125

Cys Thr Asp Ala Thr Asn Ala Thr Asn Thr Thr Ile Ile Ser Asp Met
130 135 140

Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn Met Thr Thr Glu Leu Lys
145 150 155 160

Asp Lys Thr Gln Lys Val Arg Ser Phe Phe Tyr Lys Met Asp Ile Val
165 170 175

Gln Ile Asn Asn Asp Asn Asn Ser Asn Ser Asn Ser Ser Gln Tyr Arg
180 185 190

Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
195 200 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
210 215 220

Ile Leu Lys Cys Lys Asp Lys Glu Phe Asn Gly Thr Gly Pro Cys Arg
225 230 235 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Lys Pro Val Val Ser
245 250 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Lys Val Met Ile
260 265 270

Arg Ser Glu Asn Ile Thr Asp Asn Thr Lys Asn Ile Ile Val Gln Leu
275 280 285

Thr Glu Pro Val Lys Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
290 295 300

Arg Gly Ile Ser Ile Gly Pro Gly Arg Ala Phe Ile Ala Arg Asp Arg
305 310 315 320

Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Arg Ala Ala
325 330 335

Trp Asn Asn Thr Leu Gln Lys Val Ala Gln Gln Leu Arg Thr His Phe
340 345 350

Glu Asn Arg Thr Ile Ile Phe Asn His Ser Ala Gly Gly Asp Pro Glu
355 360 365

Ile Thr Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Ser
370 375 380

Thr Thr Gly Leu Phe Asn Ser Thr Trp Ala Ser Asn Ala Ser Thr Gln
385 390 395 400

Gly Ser Asn Ser Thr Gly Ser Asn Asp Thr Ile Thr Leu Gln Cys Arg
405 410 415

Ile Arg Gln Ile Ile Arg Met Trp Gln Arg Val Gly Gln Ala Met Tyr
420 425 430

Ala Pro Pro Ile Pro Gly Val Ile Arg Cys Asp Ser Asn Ile Thr Gly
435 440 445

Leu Ile Leu Thr Arg Asp Gly Gly Asp Asn Asn Ser Thr Asn Glu Thr
450 455 460

Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu
465 470 475 480

Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr
485 490 495

Arg Ala Lys Arg Arg Val Val Glu Arg Glu Lys Arg Ala Ile Ala Gly
500 505 510

Ile Gly Ala Val Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met
515 520 525

Gly Ala Ala Ser Leu Thr Leu Thr Val Gln Thr Arg Gln Leu Leu Ser
530 535 540

Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln
545 550 555 560

Gln His Leu Leu Lys Thr Leu Val Trp Gly Ile Lys Gln Leu Gln Ala
565 570 575

Arg Val Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly
580 585 590

Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Thr Val Pro Trp
595 600 605

Asn Ser Ser Trp Ser Asn Lys Ser Tyr Ser Glu Ile Trp Asp Asn Met
610 615 620

Thr Trp Leu Gln Glu Trp Lys Glu Ile Ser Asn Tyr Thr Gln Ile Ile
625 630 635 640

Tyr Asp Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln
645 650 655

Asp Leu Leu Ala Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp
660 665 670

Ile Ser Lys Trp Leu Trp Tyr Ile Arg Ile Phe Ile Met Ile Val Gly
675 680 685

Gly Leu Ile Gly Leu Arg Ile Val Phe Ala Val Ile Ser Val Ile Asn
690 695 700

Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Leu Ala Pro
705 710 715 720

Asn Pro Gly Gly Leu Asp Arg Pro Gly Arg Ile Glu Glu Glu Gly Gly
725 730 735

Glu Gln Asp Arg Ser Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala
740 745 750

Leu Ala Trp Glu Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg
755 760 765

Leu Arg Asp Phe Ile Leu Ile Ala Ala Arg Thr Val Glu Leu Leu Gly
770 775 780

His Ser Ser Leu Lys Gly Leu Arg Leu Gly Trp Glu Gly Leu Lys Tyr
785 790 795 800

Leu Gly Asn Leu Leu Leu Tyr Trp Gly Gln Glu Leu Lys Ile Ser Ala
805 810 815

Ile Ser Leu Phe Asp Thr Ile Ala Ile Val Ile Ala Gly Trp Thr Asp
820 825 830

Arg Val Ile Glu Ile Gly Gln Arg Ile Gly Arg Ala Ile Leu Asn Ile
835 840 845

Pro Arg Arg Ile Arg Gln Gly Ala Glu Arg Ala Leu Gln
850 855 860

<210> 13
<211> 2607
<212> DNA
<213> HIV-1

<400> 13
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gggggtacctg tgtggaaaga agcaaacc actctatattt gtgcatcaga tgctaaagca 180
tatgatacag aggcacataa tgtttgggcc acacatgcct gtgtaccac agaccccaac 240

aggcagggat actcaccatt atcgtttcag acccgctcc cagcccagag gggacccgac 2220
 agggccgaag gaatcgaaga agaaggtgga gggagaggca gagacacatc cgggccatta 2280
 gtggatggat tcttagcaat tatctgggtc gacctgcgga gcctgttcct cttcagctac 2340
 caccgcttga gagacttact cttgattgta gcgaggattg tggaacttct gggacgcagg 2400
 ggggtgggaaa tcctcaagta ttggtggaat ctcctacagt attggattca ggaactaaag 2460
 aatagtgtctg ttagcttgct caacgccaca gccatagcag tagctgaggg gacagatagg 2520
 attatagaag tagcaagaag gactttttaga gctattctcc acatacctag aagaataaga 2580
 cagggttgg aaagggttt gctataa 2607

<210> 14
 <211> 866
 <212> PRT
 <213> HIV-1

<400> 14

Met Arg Val Lys Ile Lys Asn Tyr Gln His Leu Trp Arg Trp Ser Thr
 1 5 10 15

Met Leu Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu Gln Leu
 20 25 30

Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Asn Thr
 35 40 45

Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Ala His
 50 55 60

Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln
 65 70 75 80

Glu Ile Val Leu Ala Asn Val Thr Glu Asp Phe Asn Met Trp Lys Asn
 85 90 95

Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln
 100 105 110

Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn
 115 120 125

Cys Thr Asp Val Arg Asn Gly Thr Ile Val Arg Asn Ser Thr Ile Arg
 130 135 140

Val Glu Glu Gly Met Lys Glu Glu Ile Lys Asn Cys Ser Phe Asn Val
 145 150 155 160

Thr Thr Ser Met Gly Asp Lys Leu Gln Lys Glu Asp Ala Phe Phe Tyr
165 170 175

Lys Ser Asp Val Val Gln Met Gly Asp Asn Asn Asn Thr Asn Thr Ser
180 185 190

Asn Asn Asn Ile Thr Tyr Thr Ser Tyr Arg Leu Arg Ser Cys Asn Thr
195 200 205

Ser Val Ile Thr Gln Ala Cys Pro Lys Ile Asn Phe Glu Pro Ile Pro
210 215 220

Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn
225 230 235 240

Arg Thr Phe Glu Gly Lys Gly Pro Cys Lys Asn Val Ser Thr Val Gln
245 250 255

Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn
260 265 270

Gly Ser Leu Ala Glu Lys Asp Ile Val Ile Arg Ser Ala Asn Phe Ser
275 280 285

Asp Asn Ala Lys Ala Ile Ile Val Gln Leu Asn Glu Thr Val Gln Ile
290 295 300

Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Arg Ile Thr Met Gly
305 310 315 320

Pro Gly Ala Val Tyr Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile Arg
325 330 335

Arg Ala His Cys Asn Ile Ser Lys Glu Asp Trp Thr Asn Thr Leu Lys
340 345 350

Gln Ile Ala Lys Lys Leu Arg Glu Gln Phe Gly Asp Asn Lys Thr Ile
355 360 365

Ala Phe Lys Pro Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser
370 375 380

Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Thr Thr Lys Leu Phe
385 390 395 400

Asn Ser Thr Trp Phe Gly Asn Ser Thr Arg Asn Asn Thr Glu Gly Ser
405 410 415

Ser Asn Asn Gly Asn Ile Thr Leu Gln Cys Arg Ile Lys Gln Ile Ile
420 425 430

Asn Met Trp Gln Gly Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Arg
435 440 445

Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg
450 455 460

Asp Gly Gly Asn Thr Asn Asp Thr Asn Asn Thr Glu Ile Phe Arg Pro
465 470 475 480

Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
485 490 495

Lys Val Val Lys Ile Glu Pro Leu Gly Ile Ala Pro Thr Lys Ala Lys
500 505 510

Arg Arg Val Val Gln Arg Glu Lys Arg Ala Met Gly Ile Gly Ala Leu
515 520 525

Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser
530 535 540

Met Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln
545 550 555 560

Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln His His Leu Leu
565 570 575

Gln Thr Leu Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala
580 585 590

Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys
595 600 605

Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp
610 615 620

Ser Asn Lys Ser Leu Asp Lys Ile Trp Asn Asn Met Thr Trp Met Gln
625 630 635 640

Trp Glu Arg Glu Ile Asp Asn Tyr Thr Ser Leu Ile Tyr Thr Leu Ile
645 650 655

Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Leu Glu Leu Leu Glu
660 665 670

Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp Ile Thr Lys Trp
675 680 685

Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly
690 695 700

Leu Arg Ile Val Phe Val Ile Leu Ser Ile Val Asn Arg Val Arg Gln
705 710 715 720

Gly Tyr Ser Pro Leu Ser Phe Gln Thr Arg Leu Pro Ala Gln Arg Gly
725 730 735

Pro Asp Arg Pro Glu Gly Ile Glu Glu Gly Gly Gly Arg Gly Arg
740 745 750

Asp Thr Ser Gly Pro Leu Val Asp Gly Phe Leu Ala Ile Ile Trp Val
755 760 765

Asp Leu Arg Ser Leu Phe Leu Phe Ser Tyr His Arg Leu Arg Asp Leu
770 775 780

Leu Leu Ile Ala Thr Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp
785 790 795 800

Glu Ile Leu Lys Tyr Trp Trp Asn Leu Leu Gln Tyr Trp Ile Gln Glu
805 810 815

Leu Lys Asn Ser Ala Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val
820 825 830

Ala Glu Gly Thr Asp Arg Ile Ile Glu Val Ala Arg Arg Thr Phe Arg
835 840 845

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Leu Leu
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gtacctgtgt ggaaggaaac aaccaccact ctattttgtg catcagatgc taaagcatat 180

gataaagagg	tacataatgt	ttgggccaca	catgcctgtg	tacccacaga	ccccaaccca	240
caagaaatac	cattgggtaaa	tgtaacagaa	aattttaaca	tgtggaaaaa	taacatggta	300
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<400> 16

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Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Thr Thr Thr
35 40 45

Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Lys Glu Val His
50 55 60

Asn Val Trp Ala Thr Met Ala Cys Val Pro Thr Phe Pro Asn Pro Gln
65 70 75 80

Ile Val Glu Asn Phe Asn Met Leu Lys Asn Asn Met Val Glu Gln Asp
85 90 95

His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Thr
100 105 110

Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr Asp Asp Leu Arg
115 120 125

Asn Ala Asn Asn Thr Thr Thr Asn Thr Asn Ser Asn Trp Glu Lys Pro
130 135 140

Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Lys Ile Thr Ser Ser
145 150 155 160

Ile Arg Asp Lys Val Gln Lys Gln Tyr Ala Leu Phe Tyr Ser Leu Asp
165 170 175

Val Val Pro Ile Lys Asn Asn Asn Asn Ile Ser Asn Lys Ile Arg Tyr
180 185 190

Arg Leu Arg Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys
195 200 205

Val Thr Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe
210 215 220

Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Asn Gly Thr Gly Pro Cys
225 230 235 240

Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Asn Val Val
245 250 255

Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val
260 265 270

Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln
275 280 285

Leu Lys Asp Pro Val Glu Ile Asn Cys Thr Arg Pro Asn Arg Asn Ala
290 295 300

Trp Lys Gly Ile Pro Ile Gly Val Pro Gly Arg Lys Phe Tyr Ala Arg
305 310 315 320

Arg Asn Ile Thr Gly Asp Ile Arg Gln Ala Tyr Cys Asn Leu Ser Ile
325 330 335

Ala Lys Trp Thr Asn Thr Leu Lys Gln Ile Val Glu Lys Leu Arg Leu
340 345 350

His Phe Lys Asn Lys Thr Ile Val Phe Lys Ser Ser Ser Gly Gly Asp
355 360 365

Pro Glu Ile Ile Leu His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
370 375 380

Cys Asn Ser Thr Lys Leu Phe Asn Ser Thr Trp Phe Ser Thr Thr Glu
385 390 395 400

Gly Leu Asn Asn Thr Gly Asn Glu Asp Pro Ile Val Leu Pro Cys Arg
405 410 415

Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr
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Ala Pro Pro Ile Ala Asp Leu Ile Arg Cys Ser Ser Asn Ile Thr Gly
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Glu Thr Phe Arg Pro Gly Gly Gly Asn Met Arg Asp Asn Trp Arg Ser
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Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala Val
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515 520 525

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Gln Gln His Leu Leu Gln Thr Leu Val Trp Gly Ile Lys Gln Leu Gln
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Ala Arg Val Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu
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Gly Phe Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
595 600 605

Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Asp Arg Ile Trp Asn Asn
610 615 620

Met Thr Trp Met Glu Trp Glu Arg Glu Ile Asp Asn Tyr Thr Gly Leu
625 630 635 640

Ile Tyr Asn Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
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Gln Glu Leu Leu Ala Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe
660 665 670

Asp Ile Thr Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val
675 680 685

Gly Gly Leu Ile Gly Leu Arg Ile Val Phe Thr Val Leu Ser Ile Val
690 695 700

Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His His
705 710 715 720

Pro Ala Gln Arg Glu Pro Asp Arg Pro Glu Gly Ile Glu Gly Glu Gly
725 730 735

Gly Glu Arg Asp Arg Asp Arg Ser Gly Pro Leu Val Asp Gly Phe Leu
740 745 750

Ala Ile Ile Trp Val Asp Leu Arg Ser Leu Cys Ile Phe Leu Tyr His
755 760 765

Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu Leu
770 775 780

Gly Arg Arg Gly Trp Glu Val Leu Lys Tyr Trp Trp Asn Leu Leu Gln
785 790 795 800

Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Ile Asn Leu Leu Asn Ala
805 810 815

Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Ile Leu
820 825 830

Gln Arg Ala Phe Arg Ala Ile Leu His Ile Pro Thr Arg Ile Arg Gln
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Val Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Glu Ala Thr Thr Thr
35 40 45

Leu Phe Cys Ala Ser Asp Ser Lys Ala Tyr Asp Thr Glu Ala His Asn
50 55 60

Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu
65 70 75 80

Val Leu Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asp
85 90 95

Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser
100 105 110

Leu Lys Pro Cys Val Lys Leu Thr Pro Arg Cys Val Thr Leu Lys Cys
115 120 125

Thr Asp Tyr Glu Gly Asn Ala Asn Asn Thr Ile Asp Asn Ala Thr Lys
130 135 140

Asn Ser Trp Lys Gly Glu Ile Lys Asn Cys Thr Phe Asn Val Thr Thr
145 150 155 160

Ala Ile Arg Asp Lys Val Lys Lys Gln Tyr Ala Leu Phe His Ser Leu
165 170 175

Asp Val Val Pro Ile Lys Asp Ala Lys Asp Ser Asn Ser Tyr Arg Leu
180 185 190

Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val Ser
195 200 205

Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile
210 215 220

Leu Lys Cys Asn Asn Lys Thr Phe Ser Gly Lys Gly Gln Cys Lys Asn
225 230 235 240

Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Ala Ser Thr
245 250 255

Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Lys Asp Ile Ile Ile Arg
260 265 270

Ser Asp Asn Phe Ser Asp Asn Ala Lys Ile Ile Ile Val Gln Leu Lys
275 280 285

Glu Pro Val Glu Ile Asn Cys Thr Arg Pro Gly Asn Asn Thr Arg Lys
290 295 300

Ser Ile His Ile Gly Pro Gly Arg Ala Trp Tyr Ala Thr Gly Asp Ile
305 310 315 320

Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Ser Val Lys Trp
325 330 335

Asn Asn Thr Leu Arg Gln Ile Ala Lys Lys Leu Gly Glu Gln Phe Gln
340 345 350

Asp Lys Asn Ile Thr Phe Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile
355 360 365

Val Met His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ala
370 375 380

Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Gly Thr Trp Asn Asn Ser
385 390 395 400

Thr Trp Asn Glu Thr Asp Thr Thr Thr Ile Thr Leu Pro Cys Arg Ile
405 410 415

Lys Gln Ile Val Asn Met Trp Gln Thr Val Gly Arg Ala Met Tyr Ala
420 425 430

Pro Pro Ile Arg Gly Glu Ile Ser Cys Ser Ser Asn Ile Thr Gly Leu
435 440 445

Leu Leu Thr Arg Asp Gly Gly Asn Ile Asn Glu Thr Asn Gly Thr Glu
450 455 460

Ile Phe Arg Pro Ala Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu
465 470 475 480

Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Ile Ala Pro
485 490 495

Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala Val Gly
500 505 510

Val Gly Ala Met Phe Leu Gly Phe Leu Ser Ala Ala Gly Ser Thr Met
515 520 525

Gly Ala Ala Ser Val Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser
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Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln
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Gln His Leu Leu Gln Thr Leu Val Trp Gly Ile Lys Gln Leu Gln Ala
565 570 575

Arg Val Leu Ala Val Glu Arg Tyr Leu Gly Asp Gln Gln Leu Leu Gly
580 585 590

Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Thr Val Pro Trp
595 600 605

Asn Thr Ser Trp Ser Asn Lys Ser Leu Lys Tyr Ile Trp Asp Asn Met
610 615 620

Thr Trp Met Gln Trp Asp Lys Glu Ile Ser Asn Tyr Thr Gly Leu Ile
625 630 635 640

Tyr Thr Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Lys
645 650 655

Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asp
660 665 670

Ile Thr Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Ile Ile Val Gly
675 680 685

Gly Leu Ile Gly Leu Arg Ile Val Phe Thr Val Leu Ser Ile Val Asn
690 695 700

Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Arg Leu Pro
705 710 715 720

Thr Gln Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu Gly Gly
725 730 735

Glu Arg Asp Arg Asp Arg Ser Arg Thr Ser Val Asp Gly Phe Leu Ala
740 745 750

Leu Ile Trp Val Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg
755 760 765

Leu Arg Asp Leu Leu Leu Ile Leu Ala Arg Ile Val Glu Leu Leu Gly
770 775 780

Arg Arg Gly Trp Glu Thr Leu Arg Tyr Trp Trp Asn Leu Leu Gln Tyr
785 790 795 800

Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn Ser Ile
805 810 815

Ala Ile Val Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val Val Gln
820 825 830

Arg Val Cys Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg Gln Gly
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Leu Glu Arg Ala Leu Leu
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attgacaatt	acacaaatgt	aatatacaat	ttaattgaag	aatcgcagaa	ccagcaagaa	1980
aagaatgaac	aagacttatt	agcattggat	aaatgggcaa	gtttgtggga	ttgggttagc	2040
atatcaaact	ggctgtggta	tataaaaaata	ttcataatga	tagtaggagg	cttgataggt	2100
ttaagaataa	tttttactgt	actttctata	gtgaatagag	ttaggcaggg	atactcacca	2160
ttatcgtttc	agaccgcctt	cccagccccg	aggggacccg	acaggccccg	aggaatcgaa	2220
gaaggaggtg	gagagaaaga	cagagacaga	tccgggctat	tagtgaacgg	attcctttgca	2280

cttatctggg tggacctacg gagcctgtgc ctcttcagct accaccgctt gagagactta 2340
ctcttgattg cagcgagaat tgtggagctt ctgggacgca ggggggtggga aatcctcaag 2400
tattgggtgga atctcctgca gtattggagt caggaactaa agaatagtgc tgttagcttg 2460
cttaatgtca cagccatagc agtagctgag gggacagata ggattctaga agtattacaa 2520
agagcttata gagctattat tcacatacct agaagaataa gacagggctt agaaagggct 2580
ttgctataa 2589

<210> 20
<211> 862
<212> PRT
<213> HIV-1
<400> 20

Met Arg Val Lys Glu Ile Met Lys Asn Tyr Gln His Trp Trp Arg Gly
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Gly Ile Met Leu Leu Gly Leu Leu Met Ile Cys Ser Ala Ala Glu Gln
20 25 30

Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
35 40 45

Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Lys
50 55 60

His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
65 70 75 80

Gln Glu Val Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys
85 90 95

Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
100 105 110

Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
115 120 125

Asn Cys Arg Asn Val Thr Ile Thr Asn Thr Thr Thr Asn Ser Ser Gly
130 135 140

Trp Lys Leu Met Glu Glu Gly Glu Ile Lys Asn Cys Ser Phe Lys Ile
145 150 155 160

Thr Thr Ile Leu Arg His Lys Met Gln Glu Glu His Ala Leu Phe Tyr
165 170 175

Lys Ser Asp Val Val Pro Leu Gly Asn Asn Ser Ala Ile Gly Asn Asn
180 185 190

Asn Ala Arg Tyr Arg Leu Ile Ser Cys Asn Thr Ser Thr Ile Thr Gln
195 200 205

Ala Cys Pro Lys Val Thr Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
210 215 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Arg Asp Lys Lys Phe Asn Gly
225 230 235 240

Thr Gly Pro Cys Lys Asp Val Ser Thr Val Gln Cys Thr His Gly Ile
245 250 255

Lys Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
260 265 270

Glu Asp Ile Val Ile Arg Ser Ala Asn Phe Ser Asp Asn Ala Lys Ile
275 280 285

Ile Ile Val Gln Leu Asn Lys Thr Val Val Ile Asn Cys Thr Arg Pro
290 295 300

Asn Asn Asn Thr Arg Lys Gly Ile Asn Ile Gly Pro Gly Arg Thr Val
305 310 315 320

Tyr Ala Thr Gly Lys Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn
325 330 335

Ile Ser Lys Gly Glu Trp Tyr Asn Thr Leu Lys Gln Val Val Thr Lys
340 345 350

Leu Gly Glu His Phe Lys Asn Lys Thr Ile Ala Phe Asn Lys Ser Ser
355 360 365

Gly Gly Asp Pro Glu Ile Val Lys His Thr Phe Asn Cys Gly Gly Glu
370 375 380

Phe Phe Tyr Cys Asp Ser Thr Lys Leu Phe Thr Ser Thr Trp Asn Tyr
385 390 395 400

Thr Asn Gly Thr Trp Asn Ser Thr Asn Trp Asn Asp Thr Glu Met Leu
405 410 415

Asn Lys Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Val Asn Met
420 425 430

Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Leu
435 440 445

Ile Thr Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
450 455 460

Gly Ser Asn Thr Asn Thr Thr Glu Val Phe Arg Pro Gly Gly Gly Asn
465 470 475 480

Met Lys Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys
485 490 495

Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val
500 505 510

Gln Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe
515 520 525

Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Leu Thr Leu Thr
530 535 540

Val Gln Thr Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn
545 550 555 560

Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Thr Leu Val
565 570 575

Trp Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala Val Glu Arg Tyr
580 585 590

Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu
595 600 605

Ile Cys Thr Thr Thr Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser
610 615 620

Leu Asp Asp Ile Trp Asn Asn Met Thr Trp Met Glu Trp Glu Arg Glu
625 630 635 640

Ile Asp Asn Tyr Thr Asn Val Ile Tyr Asn Leu Ile Glu Glu Ser Gln
645 650 655

Asn Gln Gln Glu Lys Asn Glu Gln Asp Leu Leu Ala Leu Asp Lys Trp
660 665 670

Ala Ser Leu Trp Asp Trp Phe Ser Ile Ser Asn Trp Leu Trp Tyr Ile
675 680 685

Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg Ile Ile
690 695 700

Phe Thr Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro
705 710 715 720

Leu Ser Phe Gln Thr Arg Phe Pro Ala Pro Arg Gly Pro Asp Arg Pro
725 730 735

Glu Gly Ile Glu Glu Gly Gly Gly Glu Lys Asp Arg Asp Arg Ser Gly
740 745 750

Leu Leu Val Asn Gly Phe Phe Ala Leu Ile Trp Val Asp Leu Arg Ser
755 760 765

Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Ala
770 775 780

Ala Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ile Leu Lys
785 790 795 800

Tyr Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser
805 810 815

Ala Val Ser Leu Leu Asn Val Thr Ala Ile Ala Val Ala Glu Gly Thr
820 825 830

Asp Arg Ile Leu Glu Val Leu Gln Arg Ala Tyr Arg Ala Ile Ile His
835 840 845

Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ala Leu Leu
850 855 860

<210> 21

<211> 2598

<212> DNA

<213> HIV-1

<400> 21

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gtgtggagag acgcagagac caccttattt tgtgcatcag atgctaaagc atatgataca	180
gaagtacata atgtttgggc tacacatgcc tgtgtaccca cagaccctaa cccacaagaa	240
atacctttgg aaaatgtaac agaaaatttt aatatgtgga aaaataacat ggtagagcag	300

gagcaagaca gagacaggtc cgtgagatta gtgaacggat tcttagctct tgcctgggac 2280
gatctacgga gcctgtgcct cttcagctac caccgattga gagacttact cttgattgca 2340
gcgaggactg tggaacttct gggacacagc agtctcaagg gactgagact ggggtgggga 2400
gccctcaa atctgtggaa tcttctgtca tactggggcc aggaactaaa gaatagtgt 2460
attaatctgc ttgatacaac agcaatagca gtagctaatt ggacagacag agttatagaa 2520
ataggacaaa gatttggtag agctattctc aatataccta gaagaatcag acagggcctc 2580
gaaagggctt tgcaataa 2598

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<211> 864
<212> PRT
<213> HIV-1

<400> 22

Met Arg Val Lys Thr Gln Lys Ser Tyr Pro Leu Leu Trp Arg Trp Gly
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Ile Ile Phe Trp Ile Met Val Ile Cys Asn Ala Glu Asn Leu Trp Val
20 25 30

Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Asp Ala Glu Thr Thr Leu
35 40 45

Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His Asn Val
50 55 60

Trp Ala Thr His Ala Cys Val Pro Thr Phe Pro Asn Pro Gln Glu Ile
65 70 75 80

Pro Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
85 90 95

Val Glu Gln Met His Glu Asp Ile Ile Ser Asp Trp Asp Gln Ser Leu
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr
115 120 125

His Asn Phe Asn Asn Phe Asn Ser Ser Asn Asn Ser Thr Pro Ile Asn
130 135 140

Asn Thr Ile Tyr Asn Gly Met Gln Gly Glu Ile Lys Asn Cys Ser Phe
145 150 155 160

Asn Thr Thr Thr Glu Leu Arg Gly Lys Thr Lys Lys Gln Tyr Ala Leu

165

170

175

Phe Asn Lys Leu Asp Val Val Gln Ile Asn Asp Lys Asn Asn Ser His
180 185 190

Ser Asn Asn Arg Arg Tyr Met Leu Ile His Cys Asn Thr Ser Val Ile
195 200 205

Thr Gln Ala Cys Pro Lys Val Thr Phe Glu Pro Ile Pro Ile Tyr Tyr
210 215 220

Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Lys Asp Gln Glu Phe
225 230 235 240

Asn Gly Ser Gly Pro Cys Asn Asn Val Ser Thr Val Gln Cys Thr His
245 250 255

Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu
260 265 270

Ala Glu Arg Lys Ile Met Ile Arg Ser Glu Asn Ile Thr Asn Asn Ala
275 280 285

Lys Thr Ile Ile Val Gln Phe Thr Glu Pro Val Glu Ile Asn Cys Thr
290 295 300

Arg Pro Asn Asn Asn Thr Arg Lys Arg Val Gly Val Gly Pro Gly Arg
305 310 315 320

Ala Val Tyr Val Thr Asn Ala Ile Ile Gly Asp Ile Arg Gln Ala Tyr
325 330 335

His Asn Val Ser Arg Ala Lys Trp Asn Asp Thr Leu Lys Lys Val Val
340 345 350

Thr Gln Leu Arg Lys His Phe Asn Thr Thr Ile Val Phe Thr Lys Pro
355 360 365

Ser Gly Gly Asp Val Glu Ile Thr Thr His Ser Phe Asn Cys Gly Gly
370 375 380

Glu Phe Phe Tyr Cys Asn Thr Ser Gln Leu Phe Asn Ser Thr Trp Ile
385 390 395 400

Ile Asn Gly Thr Asn His Thr Gly Pro Tyr Asp Thr Asp Thr Ile Thr
405 410 415

Leu Arg Cys Arg Ile Lys Gln Ile Val Lys Thr Trp Gln Arg Val Gly
420 425 430

Gln Ala Met Tyr Ala Pro Pro Ile Pro Gly Val Ile Arg Cys Asp Ser
435 440 445

Asn Ile Thr Gly Ile Leu Leu Thr Arg Asp Gly Gly Lys Ile Asn Ser
450 455 460

Thr Asn Glu Thr Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp
465 470 475 480

Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly
485 490 495

Val Ala Pro Thr His Ala Lys Arg Arg Val Val Glu Arg Glu Lys Arg
500 505 510

Ala Val Gly Val Ile Gly Ala Val Phe Leu Gly Phe Leu Gly Ala Ala
515 520 525

Gly Ser Thr Met Gly Ala Ala Ala Ile Thr Leu Thr Val Gln Ala Arg
530 535 540

Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala
545 550 555 560

Ile Glu Ala Gln Gln His Leu Leu Lys Thr Leu Val Trp Gly Ile Lys
565 570 575

Gln Leu Gln Ala Arg Val Leu Ala Leu Glu Arg Tyr Leu Arg Asp Gln
580 585 590

Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr
595 600 605

Asn Val Pro Trp Asn Ser Ser Trp Ser Asn Lys Thr Phe Asn Asp Ile
610 615 620

Trp Asn Met Thr Trp Leu Gln Trp Asp Lys Glu Ile Asn Asn Tyr Thr
625 630 635 640

Asn Thr Ile Tyr Arg Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys
645 650 655

Asn Glu Gln Asp Leu Leu Ala Leu Asp Lys Trp Ala Ser Leu Trp Ser
660 665 670

Trp Phe Asp Leu Ser Asn Trp Leu Trp Tyr Ile Arg Ile Phe Ile Met
675 680 685

Val Val Gly Gly Leu Ile Ala Leu Arg Ile Val Phe Ala Val Leu Ala
690 695 700

Ile Ile Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr
705 710 715 720

Leu Thr His His Gln Arg Glu Pro Asp Arg Pro Glu Gly Ile Glu Glu
725 730 735

Gly Gly Gly Glu Gln Asp Arg Asp Arg Ser Val Arg Leu Val Asn Gly
740 745 750

Phe Leu Ala Leu Ala Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser
755 760 765

Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Ala Ala Arg Thr Val Glu
770 775 780

Leu Leu Gly His Ser Ser Leu Lys Gly Leu Arg Leu Gly Trp Gly Ala
785 790 795 800

Leu Lys Tyr Leu Trp Asn Leu Leu Ser Tyr Trp Gly Gln Glu Leu Lys
805 810 815

Asn Ser Ala Ile Asn Leu Leu Asp Thr Thr Ala Ile Ala Val Ala Asn
820 825 830

Trp Thr Asp Arg Val Ile Glu Ile Gly Gln Arg Phe Gly Arg Ala Ile
835 840 845

Leu Asn Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ala Leu Gln
850 855 860

<210> 23
<211> 24
<212> DNA
<213> Primer

<400> 23
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24

<210> 24
<211> 24
<212> DNA
<213> Primer

<400> 24
gtccccagcg gaaagtcct tgta

24

<210> 25
<211> 25
<212> DNA
<213> Primer

<400> 25
gagacagtgg caatgagagt gaagg

25

<210> 26
<211> 26
<212> DNA
<213> Primer

<400> 26
ctttttgacc acttgccacc catctt

26

<210> 27
<211> 7
<212> PRT
<213> Peptide

<400> 27
His Ser Ser Leu Lys Gly Leu
1 5